

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 05:23:17 ; Search time 8805 Seconds

(without alignments)  
11214.184 Million cell updates/sec

Title: US-09-679-687B-1

Perfect score: 2088

Sequence: 1 gcacgagacactcctcacct.....aaaaaaaaaaaaaaaaaaaaa 2088

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgs.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1320.6	63.2	1834	8 AB008464	AB008464 Zea mays
2	1073.8	51.4	2021	8 AF408843	AF408843 Triticum
3	1070.6	51.3	2134	8 AF408842	AF408842 Triticum
4	1070.6	51.3	2160	8 BT009324	BT009324 Triticum
5	1062.6	50.9	2044	8 HVT0272309	AJ272309 Hordeum v
6	1058.8	50.7	2106	8 AF408844	AF408844 Triticum
7	1053	50.4	2083	8 BT009233	BT009233 Triticum
8	1021	48.9	2062	8 AK100027	AK100027 Oryza sat
9	1016.8	48.7	2036	8 D87819	D87819 Oryza sativ
10	958.2	45.9	1580	6 AX653870	AX653870 Sequence
11	812	38.9	1713	8 AB071809	AB071809 Oryza sat
12	745.8	35.7	17340	2 AC149831	AC149831 Zea mays
13	608.6	29.1	2036	8 AK073105	AK073105 Oryza sat
14	603.8	28.9	1972	8 AB091674	AB091674 Oryza sat
15	566	27.1	1222	8 AK109355	AK109355 Oryza sat
16	474.6	22.7	1072	8 BT009200	BT009200 Triticum
17	397	19.0	1830	8 AV137242	AV137242 Oryza sat
18	395.4	18.9	2158	8 AB091673	AB091673 Oryza sat
19	385.6	18.5	2166	8 AY581895	AY581895 Zea mays

20	368.6	17.7	1800	8 PMA534442	AJ534442 Plantago
21	348.6	16.7	2386	8 AY098894	AY098894 Citrus si
22	330.8	15.8	1638	6 AX654482	AX654482 Sequence
23	327.2	15.7	1785	6 AX259876	AX259876 Sequence
24	327.2	15.7	1785	6 AX507014	AX507014 Sequence
25	327.2	15.7	1785	6 AX651257	AX651257 Sequence
26	327.2	15.7	1785	8 ATH289165	ATH289165 Arabidops
27	323.6	15.5	2137	8 AF166498	AF166498 Lycopersi
28	316	15.1	2130	8 AF021809	AF021809 Vitis vin
29	315	15.1	1818	6 AX259902	AX259902 Sequence
30	315	15.1	1818	8 AY291289	AY291289 Solanum t
31	300.2	14.4	2558	8 AK065430	AK065430 Oryza sat
32	292.4	14.0	2018	8 HVT0272308	HVT0272308 Hordeum v
33	290.8	13.9	2135	6 AX306541	AX306541 Sequence
34	284.2	13.6	1796	8 AB036758	AB036758 Daucus c
35	276.2	13.2	63167	8 AC090487	AC090487 Genomic s
36	276.2	13.2	173374	8 AC146340	AC146340 Genomic s
37	276.2	13.2	305960	8 AE017092	AE017092 Oryza sat
38	271.6	13.0	7518	8 AF419298	AF419298 Oryza sat
39	271.4	13.0	1858	8 DCSUT2	Y16768 Daucus caro
40	268.8	12.9	1925	8 AF021810	AF021810 Vitis vin
41	266.2	12.7	408	8 AF378185	AF378185 Oryza sat
42	263.2	12.6	405	8 AF378186	AF378186 Oryza sat
43	252.8	12.1	1906	8 AY065839	AY065839 Brassica
44	249.6	12.0	289	11 BV137381	BV137381 PZA00076
45	249.6	12.0	289	11 BV137384	BV137384 PZA00076

## ALIGNMENTS

RESULT 1  
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LOCUS AB008464 1834 bp mRNA linear PLN 23-MAY-2003  
DEFINITION Zea mays mRNA for Sucrose Transporter, complete cds.  
ACCESSION AB008464  
VERSION AB008464.1 GI:5771353  
KEYWORDS Sucrose Transporter.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1  
Aoki,N., Hirose,T., Takahashi,S., Ono,K., Ishimaru,K. and Ohsugi,R.  
Molecular cloning and expression analysis of a gene for a sucrose transporter in maize (Zea mays L.)  
Plant Cell Physiol. 40 (10), 1072-1078 (1999)  
20058970  
FUBMED 10589520  
REFERENCE 2 (bases 1 to 1834)  
Aoki,N.  
Direct Submission  
Submitted (24-OCT-1997) Naohiro Aoki, Japan International Research Center for Agricultural Sciences, Biological Resources Division; 1-2 Ohwashi, Tsukuba, Ibaraki 305, Japan  
E-mail:naoki@res.jircas.affrc.go.jp, Tel:81-0298-38-6305, Fax:81-0298-38-6650)  
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## FEATURES

source

gene

CDS



FEATURES	1600, Canberra, ACT 2601, Australia	
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Query Match	51.4%; Score 1073.8; DB 8; Length 2021;	
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Matches 1277; Conservative	0; Mismatches 317; Indels 3; Gaps 1;	
QY	187	ACGTGTGTCTCGCCATGCTCGTGGCGACGCGGCGAGCTGGCGGAGCTGTCCGCGGGG 246
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QY	247	GTCGCGGGCGCGCGCGGTGTGACACGATGGCCCGCGATCAGCTCGGAGGCTCATC 306
Db	181	GGCGCGCGCGCGCGGCGGACCCCGCCCGGTGGACATCAGCTCGGAGGCTCATC 240
QY	307	CTCGCGGCGATGTCGCGCGCGCGGTGCAGTACGGCTGGGCGCTGCAGCTCTCCCTCTC 366
Db	241	CTCGCGGCGATGTCGCGCGCGCGGTGCAGTACGGATGGGCGCTCCAGCTCTCCCTCTC 300
QY	367	AGCCCTACGTGACAGCTCTGGGCTTTCAATGCGGTCACTTCAATGAGTCTGCTG 426
Db	301	ACCCTACGTGACAGCTCTGGGCTTTCAATGCGGTCACTTCAATGAGTCTGCTG 360
QY	427	GGCCCTATTCGGGCTTAGTGTCCAAACCGCTGTTGTCCTGTGTCGAGCAGAGTGACA 486
Db	361	GGCCCTATTCGGATTTAGTGTTCACCATCGGTGGGCTCTACGTGACAGTGCACT 420
QY	487	TGAGATGGGGAGACGAGGCGCGTTTATCTGACAGGCTGCATGCTCATCTGGTTGCC 546
Db	421	TCTAGATGGGAAAGACGACGACCGTTTATCTGACAGGATATATCTTCATCTGCAATTGCT 480
QY	547	GTCATTTGTCGGATTTCTGTCAGACATCGAGTGTCTTAGGGGACAGAGGAACAC 606
Db	481	GTCGTAGTCGTGGGCTTCTCGGCTGACATTTGGAGTGTCTGTTGGTGACAGAGGAAG 540
QY	607	TGACGCTCTACCAAGTCTCTGTTGGACGCTGCGATCGTGTACGTTCTGGGCTTTTGG 666
Db	541	TGCACTCTCTATCATGCGGCTCTGTTGGACCGCTGCAATTTGTATGTTCTTGATTTCTGG 600
QY	667	CTCCTTGACTTCTCCAAACACACTGTGCGAGGTCAGACGTCGTATGATGCTGATCTA 726
Db	601	CTCCTTGACTTCTCCAAACACACTGTGCGAGGTCAGCGGCTGCTGATGGCTGATTTA 660
QY	727	TGTGACCATCATGGSCCAAGTGGGCTAACTCCATCTTCTGTTCTTGGATGGGCTGGGA 786
Db	661	TCAGCTCAACATGACCCAGTGCAGCAAAATCAATCTTCTGTTCTTGGATGGCACTAGGA 720
QY	787	AACATCTTAGGCTACTCTCTGGTTCACGACAAATTTGGACAAAGTGTTCCTTCCCTT 846
Db	721	AATATCTTGGATCTCTCTGGTTCACAAATTAATGGCACAAAGTGTTCCTTCCCTC 780
QY	847	AAACGAGCGCTGCTGTGAGGCTGTGCGAACCTGAAAGGTGCAATTTCTTGTTGGCGGTG 906
Db	781	CGGACAGGGCTTGTCTGAGGCTGCGCAAACTGAAAGGCGCATTTCTTGTTGGCGAGTG 840
QY	907	GTGTTCTAGTCTGTGCTGACGTTAACTCTGATCTTCCCAAGAGGTCCTGATCAGA 966
Db	841	CTGTTCTGCGCTTCTGTTGGTGATAAATGATGATCTTCCCAAGAGATACCGTACAAG 900
QY	967	GCAGAACAGAACCTCCCGACGACGAGGCGCGGCGAGCTCGAGCTGAGCTACCGG 1026
Db	901	GCATTCGCGCCCTCC---CAACAAGGCCAATGGCAGGTTGAAGTCGAGCCCACTGGG 957
QY	1027	CCACTTCCGCTGCTCAAGGCTTCAAGGACCTCCCTCCCGGGATGCGCTCGTCTCTCTC 1086
Db	958	CCGCTCCGCTGTTCAAGAGCTTCAAGAACTTGCCTCTCTGGAATGCCATCAGTGTCTCTC 1017
QY	1087	GTGATCTCCATCACTTGGCTTTCGTGTTCCCTCTTATCTCTACGACACGACTGGATG 1146
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QY	1147	GGCGGGGAGATCTACCAACGCGGACCCCAAGGGGAGCAAGCCCAAGATCTCGGCTTCAAC 1206
Db	1078	GGTCTGAGATCTACCAAGGCTGACCCCAAGGGAACCCCGACGAGGCCAAGCTTCCAG 1137
QY	1207	GAAGTGTCCGAGTTCGCGCGGTTTGGGCTGCTACTCAACTCGGTTATTTAGGTTTCAAG 1266
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QY	1267	TCGTTCTCTGATCGAGCCCATGTCCCGAAGGTTCGCGCGGAGGTGTGTGGGTGACGAGC 1326
Db	1198	TCCTTCTGATCGAGCGCTGTGCAAGAGGTAGGCGCGGCTGTGTGGGTGTGAGC 1257
QY	1327	AACCTCATGTTCTGCTGCGCTATGGCGGCAACCGCTGATCAGCTTCTGTTGCTCTCAGG 1386
Db	1258	AACCTCTCTGCTGCGCTCTCCATGGGCGGCAATTTGCATCATAGCTTGTGGGTACTCAG 1317
QY	1387	GACTACACGGGTACGTGACGAGGACCATCACCGGAAACCCAGCATCAAGGCGCTGTC 1446
Db	1318	GATGATGGGTACATCCAGACGCGCATCACCGCAGCAAGAGATCAAGATCGTCTCTC 1377
QY	1447	CTCGTCTCTTTCGCTTCTGCGGCTTCTGCGGCTTCTGCGCATCTGTACAGCTTCCGCTTCCGG 1506
Db	1378	CTCGGCTCTTTCGCTTCTGCGGCTTCTGCGGCTTCTGCGCATCTGTACAGTGTCTCTTCCGG 1437
QY	1507	GTACCGGCGAGTGGCGGCGCCACCGGCGGCGGCGGCGGCGGCTGTGACCGGCTCTC 1566
Db	1438	GTACCGGCGAGTGGCGGCGCAACAGAGCGGTGGCCAAAGGCTGTGCAACGCGGCTGCTG 1497
QY	1567	AACATCTCCATCTGTCATCTCCCTCAGGTGATCATCGGCTGCGGCGCGGCGGCGGCGGCGG 1626
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QY	1627	CTGTTCCGGAAGGCAACATCCCGGCGGTTTCGCGGCTGCGGCTTCCGCTTCCGCTTCCGCT 1686
Db	1558	CTGTTCCGGAAGGCAACATCCCGGCGGTTTCGCGGCTGCGGCTTCCGCTTCCGCTTCCGCT 1617
QY	1687	GGGCTGTTGGGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1746
Db	1618	GGGCTGTTGGGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1746
QY	1747	GGGCGGCGCATGTATCGAAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1783
Db	1678	GGGCGGCGCATGTATCGAAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1714
RESULT 3		
LOCUS	AF408842	
DEFINITION	Triticum aestivum sucrose transporter SUT1A mRNA, complete cds.	
ACCESSION	AF408842	
VERSION	AF408842.1	
KEYWORDS	GI:20152870	
SOURCE	Triticum aestivum (bread wheat)	
ORGANISM	Triticum aestivum	



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QY 1747 GCGGGCGGCACTGATCGAACCAGCGCGCGCGCGCGCC 1783
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1776 GCGGGCGGTCACTGACCGCGCGCGCGCGCGCGCGCGCC 1812

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LOCUS Triticum aestivum clone wlm24.pk0015.gll.fis, full insert mRNA
DEFINITION
sequence.
ACCESSION BT009324
VERSION BT009324.1 GI:32128875
KEYWORDS FLI CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 2160)
AUTHORS Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
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197 ACGATGGCGCGCGCGCGCGCAACGGCGAGGTGGAGCTCTCGTGGGGTGGCGGAGGC 256
QY 247 GTCCGGCGCGCGCGCGGTGTGGACACGTCGTGGCGCCGATCAGCTCGGAGGCTATC 306
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317 CTCGCGCGCATGCTGCCGCGCGCGTGCAGTACGATGGGCGCTCCAGCTCTCCCTGCTC 376
QY 367 AGCGCCCTAGCTCAGACTCTGGGGCTTTCAATGCGCTCACTTCAATGAGCTGTGC 426
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
377 ACCCCCTAGCTCCAGACTCGGGACTTTTCGATGCTCTGACTTCAATTCATGAGCTGTC 436
QY 427 GCGCCCTATTGCGCGCTTAGTGTCACACCGCTGTGGCTTGCCTGTACAGGGTGATGCTCATCTGGGTTGCC 486
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
437 GCGCCCTATTGCTGGATTAGTGTTCAACATGCGTGGGCTCTCAGTGAACAAGTCACT 496
QY 487 TCGAGATGGGGAGACGAGGCGCTTTATCTTCACAGGGTGATGCTCATCTGGGTTGCC 546
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497 TCAAGATGGGAAGACGACAGACCGTTCAATCTGACAGGATGATCTCTCATCTGATTTGCT 556
QY 547 GTCATTGTGTCGATTCTCGTCAGACATCGGAGCTGCTTAGGGGACACGAAGAACAC 606
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557 GTCGTGTCGTGGCTTCTCGGCTGACATTTGAGTGTCTCTGGGTGACAGCAAGGAAGAG 616
QY 607 TGCAGCTCTACCAAGCTCTCGTGTGGCACGCTGCGATCGTGTAGCTTCTGGGTTTGG 666
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617 TGCAGCTCTATCATATGCGGCTCGTTGGCACTGCAATTTGTATGTTCTTGGATTCTGG 676
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677 CTCCTTGACTTCTCCAAACAACAGTGCAGGACCGCGCTGCTCTGATGGCTGATTTA 736

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RESULT 5  
 HVU272309      2044 bp      mRNA      linear      PLN 22-FEB-2000  
 LOCUS      Hordeum vulgare mRNA for sucrose transporter 1 (sut1 gene).  
 DEFINITION  
 ACCESSION      AJ272309  
 VERSION      GI:7024414  
 KEYWORDS      sucrose transporter; sut1 gene.  
 SOURCE      Hordeum vulgare subsp. vulgare  
 ORGANISM      Hordeum vulgare subsp. vulgare  
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
                  Pooideae; Triticeae; Hordeum.  
 REFERENCE      1      Weschke, W., Panitz, R., Sauer, N., Wang, Q., Neubohn, B., Weber, H. and  
 AUTHORS      Wobus, U.  
 TITLE      Sucrose transport into Barley Seeds: Molecular Characterisation of  
                  two Transporters and Implications for Seed Development and Starch  
                  Accumulation  
 JOURNAL      Unpublished  
 REFERENCE      2      (bases 1 to 2044)  
 AUTHORS      Weschke, W.  
 TITLE      Direct Submission  
 JOURNAL      Submitted (21-FEB-2000) Weschke W., Molecular Genetics, Institut  
                  fuer Pflanzen-genetik und Kulturpflanzenforschung, Corrensstr.5,  
                  Gatersleben 06466, GERMANY  
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                  Query Match      50.9%;      Score 1062.6;      DB 8;      Length 2044;  
                  Best Local Similarity      80.0%;      Pred. No. 1.4e-139;  
                  Matches 1277;      Conservative      0;      Mismatches 314;      Indels      6;      Gaps      2;  
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 Db      124      CCCTGCGATGGCGCGCGCGGCACACGCGAGGTGGAGCTCTCGTGGGGTGGCGG 183  
 QY      243      GGGGTTTCG 299  
 Db      184      CGAGGCG 243  
 QY      300      GTCATCTCTCGCGCGCATGTGTGCGCGGCGCGGTGCAGTACGGTGGCGCTGCAGCTCTC 359  
 Db      244      GCTCATCTCTCGCGCGCATGTGTGCGCGGCGCGGTGCAGTACGGATGGCGCGCATCTCTC 303





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Db      1300 GTTCAGCTCGTTCTGATCGAGCCGCTGTGCAAGAGGCTAGGCCCGCGGTGTGGT 1359
Qy      1320 GACGAGCACTTATGTTCTGCTGCGTCATCGGCGCCACCGCGTATGATGCTTCTGGTC 1379
Db      1360 GTCGAGCAACTTCTCTGCTGCTCTCCATGCGCGCGGATTGGAATATAAGCTTGTGGGC 1419
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Db      1540 TTTGCGGTGTACGCGGCTAGTGTGCGGCGCAAGAGAGCGGTGGCCAGGCTGTGACGGG 1599
Qy      1560 GGTCTCAACATCTCATCTGCTATCCCTCAGGTGATCATCGCGTGTGGCGCGCGCGGTG 1619
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Qy      1620 GGAGCGCTGTGTGCGGAGGCAATCCCGCGTGTGCGGCTGCGGCTGTGCGGCT 1679
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Qy      1680 GGTGCGGCGGTGTGCGGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1739
Db      1720 CATCGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1779
Qy      1740 GGTGCGGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1797
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RESULT 7
LOCUS   BT009233
DEFINITION   Triticum aestivum clone wleln.pk0103.c11:fls, full insert mRNA
ACCESSION   BT009233
VERSION     BT009233.1 GI:32128784
KEYWORDS    FLI CDNA.
SOURCE      Triticum aestivum (bread wheat)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE  1 (bases 1 to 2083)
AUTHORS   Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
TITLE      Direct Submission
JOURNAL    Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
FEATURES
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         /db_xref="taxon:4565"
         /clone="wleln.pk0103.c11:fls"

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Query Match      50.4%; Score 1053; DB 8; Length 2083;
Best Local Similarity 80.2%; Pred. No. 3.2e-138;
Matches 1249; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

Qy      240 CGCGGGGTTCGCGCGCGCGCGCGGTGTGTGACCACTGTCGCCCGCATCAGCTTCGGGAG 299
Db      269 CGAGGCGCGCGCGCGCGCGCGGTGTGTGACCACTGTCGCCCGCATCAGCTTCGGGAG 328
Qy      300 GGTCTATCTTCGCGCGGTGTGTGCGCGCGGTGTGTGACCACTGTCGCCCGCATCAGCTTC 359

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Db      329 ACTCATCTCCGCGGCATGTGTCGCGCGCGGTGTGCAAGTACGATGGGCGCTCCAGTCTC 388
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Db      389 CCTGCTACCCCTACGTCCAGACTCTGGACTTTCGATGCTCTGACTTCAATCAATGTG 448
Qy      420 GCTTGGCGCTATGTGCGGCTTAGTGTCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
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Qy      480 GTGTACATCGAGATGGGAGACGAGGCGCTTTATCTGACAGGCTGCTCATCTG 539
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Qy      540 GTTTCGCTCATGTGTGCGGATTTCTGTCAGACATCGAGCTGCTTAGGGGACAGAA 599
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Qy      600 GGAAACATGACGCTTACACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
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Qy      660 GTTTCGCTCATGTGTGCGGATTTCTGTCAGACATCGAGGCTGCTGCTGCTGCTGCTGCTGCT 719
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Qy      1080 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139
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Qy      1320 GACGAGCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1379
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Qy      1380 GCTCAGGAGTACAGCGGTACGTGAGGACCGCATCAGCGGAGCCAGCATCAAGGC 1439
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 Db 1586 CCGTCGCTCAACATCTCGATCTGTCATCCCGCAGTGATCGCGTGGCGCGGCCCGCTG 1645  
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 Db 1706 CATCGCGCGCATCTGCGCGCATATCTGCTGCCAAGATCTCCAGCGCCAGTTCGCGGC 1765  
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## RESULT 8

AK100027

LOCUS

DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J013146J01, full insert sequence.

AK100027

ACCESSION

AK100027.1 GI:32985236

VERSION

FLI CDNA; CAP trapper.

KEYWORDS

Oryza sativa (japonica cultivar-group)

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1

The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yarak, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Ohtsuki, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Arakawa, T., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Ohtsuki, K., Itoh, M., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

JOURNAL

Science 301 (5631), 376-379 (2003)

MEDLINE

22752273

PUBMED

12869764

REFERENCE

2 (bases 1 to 2062)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashidume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,

Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oota, N., Ota, Y., Ohtsuki, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

## Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: shikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashidume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

## FEATURES

Location/Qualifiers

1..2062

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="J013146J01"

## ORIGIN

Query Match 48.9%; Score 1021; DB 8; Length 2062;  
 Best Local Similarity 78.1%; Pred. No. 1e-133;  
 Matches 1232; Conservative 0; Mismatches 330; Indels 3; Gaps 1;

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QY 311 CGGGCATGCTCGCGCGCGCGTGCAGTACGGCTGGGCGCTGCAGCTCTCCCTCCCTCACGC 370  
 Db 367 CCGGATGCTCGCGCGCGCGCTGCAGTACGGCTGGGCGCTGCAGCTCTCCCTCCCTCACCC 426

QY 371 CTTAGCTGAGACTCTGGGGCTTTTCAATGCGCTCACTTCATTCATGTTGCTCTCGGCGC 430  
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QY	551	TTGTTGTCGGAATCTCGTCAGACATCGAGCTGCTCTAGGGGACACGAAGACACATGCA	610
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Db	1027	ATGACGCGCTCCCAAC---AAATCAAACGAGCAGCTGAGCCTGAAGCACTGGTCCAC	1083
QY	1031	TTGCGCTCTCAAGGGCTTCAAGACCTGCTCCCGGATGCCGCTCGCTCTCTCTGTGA	1090
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RESULT	9
LOCUS	D87819
DEFINITION	Oryza sativa (japonica cultivar-group) mRNA for sucrose transporter, complete cds.
ACCESSION	D87819
VERSION	D87819.1
KEYWORDS	GI:2723470
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	1 Hirose, T., Imaizumi, N., Scofield, G. N., Furbank, R. T. and Ohsugi, R. cDNA cloning and tissue specific expression of a gene for sucrose transporter from rice (Oryza sativa L.) Plant Cell Physiol. 38 (12), 1389-1396 (1997)
JOURNAL	98182940
MEDLINE	9522469
REFERENCE	2 (bases 1 to 2036)
AUTHORS	Hirose, T.
TITLE	Direct Submission
JOURNAL	Submitted (09-SEP-1996) Tatsuro Hirose, Hokuriku National Agricultural Experiment Station, Lab. of Rice Metabolism; 1-2-Iinada, Joetsu, Niigata 943-01, Japan
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Query Match 45.9%; Score 958.2; DB 6; Length 1580;  
Best Local Similarity 77.4%; Pred. No. 6.4e-125;

Matches 1199; Conservative 0; Mismatches 323; Indels 27; Gaps 2;

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 KEYWORDS Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 SOURCE Oryza sativa (japonica cultivar-group)  
 The sucrose transporter gene family in rice  
 Plant Cell Physiol. 44 (3), 223-232 (2003)

REFERENCE  
 AUTHORS Aoki, N., Hirose, T., Scofield, G.N., Whitfield, P.R. and Furbank, R.T.  
 TITLE The sucrose transporter gene family in rice  
 JOURNAL Plant Cell Physiol. 44 (3), 223-232 (2003)  
 MEDLINE 22555500  
 PUBMED 12688768  
 REFERENCE  
 AUTHORS Hirose, T., Scofield, G.N., Whitfield, P.R., Aoki, N., Furbank, R.T. and Terao, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-SEP-2001) Tatsuhiro Hirose, National Agricultural Research Center, Department of Rice Research; 1-2-1 Inada, Joetsu, Niigata 953-0193, Japan (E-mail: dragon@affrc.go.jp, Tel:81-255-26-8300, Fax:81-255-24-8578)

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ORGANISM Zea mays

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clade; Panicoideae; Andropogoneae; Zea.  
AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.  
and Wessing, J.  
Ze mays, clone ZMMB0408K22  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 173340)  
AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.,  
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,  
Arachchi, H.M., Barua, N., Bastien, V., Bloom, T., Boguslavskiy, L.,  
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Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S.,  
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Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997).  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/MIT Center for Genome Research  
Center code: WIPR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@broad.mit.edu](mailto:sequence_submissions@broad.mit.edu)

Bharti, AK and Messing, J: The Plant Genome Initiative at  
Rutgers, Waksman Institute, Rutgers, The State University of New  
Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
(<http://psir.rutgers.edu>)  
Butler, E and Wing, R: Arizona Genomics Institute, Biological  
Sciences West, 448A, P.O. Box 210088, University of Arizona,  
Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)

----- Project Information -----  
Center project name: L30302  
Center clone name: 408\_K\_22

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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AB091674			
VERSION			
AB091674.1 GI:29467455			
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ORGANISM			
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Oryza sativa (japonica cultivar-group)			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.			
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1			
Aoki, N., Hirose, T., Scofield, G.N., Whitfield, P.R. and Furbank, R.T. The sucrose transporter gene family in rice			
Plant Cell Physiol. 44 (3), 223-232 (2003)			
MEDLINE			
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PUBMED			
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2 (bases 1 to 1972)			
Hirose, T., Aoki, N., Scofield, G.N., Whitfield, P., Furbank, R.T. and Terao, T.			
Direct Submission			
Submitted (13-SEP-2002) Tatsuro Hirose, National Agricultural Research Center, Department of Rice Research; 1-2-1 Inada, Joetsu, Niigata 943-0193, Japan (E-mail: dragon@affrc.go.jp, Tel:81-25-526-8300, Fax:81-25-524-8578)			
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 LOCUS  
 DEFINITION  
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AKI09355  
 VERSION  
 AKI09355.2 GI:42821672

KEYWORDS  
 FLI\_CDNA; oligo capping.

SOURCE  
 Oryza sativa (japonica cultivar-group)

ORGANISM  
 Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 The Rice Full-length cDNA Consortium, National Institute of

Agricultural Sciences Rice Full-length cDNA Project Team,

Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,

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Collection, mapping, and annotation of over 28,000 cDNA clones from

japonica rice

Science 301 (5631), 376-379 (2003)

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PUBMED

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C 44	69	3.3	3410	4	US-09-115-453-110	Sequence 110, App
C 45	69	3.3	3410	4	US-09-688-489-110	Sequence 110, App

## ALIGNMENTS

RESULT 1  
US-08-356-340-1  
; Sequence 1, Application US/08356340  
; Patent No. 5608146  
; GENERAL INFORMATION:  
; APPLICANT: FROMMER, Wolf-Bernd  
; APPLICANT: RISMAYER, Jorg  
; TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE  
; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A  
; TITLE OF INVENTION: TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND  
; TITLE OF INVENTION: TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFI...  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oetolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/356,340  
; FILING DATE: 21-DEC-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/EP93/01604  
; FILING DATE: 22-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P42 20 759.2  
; FILING DATE: 24-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meilman, Edward A.  
; REGISTRATION NUMBER: 24,735  
; REFERENCE/DOCKET NUMBER: P/951-106  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 382-0700  
; TELEFAX: (212) 382-0888  
; TELEX: 236925  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1969 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:



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## RESULT 3

US-08-356-340-3

; Sequence 3, Application US/08356340

; Patent No. 5608146

; GENERAL INFORMATION:

; APPLICANT: FROMMER, Wolf-Bernd

; APPLICANT: RIESMEIER, Jorg

; TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE

; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A  
; TITLE OF INVENTION: TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND  
; TITLE OF INVENTION: TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFI...

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ostrolenk, Faber, Gerb &amp; Soffen

; STREET: 1180 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10036-8403

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,340

; FILING DATE: 21-DEC-1994

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US PCT/EP93/01604

; FILING DATE: 22-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P42 20 759.2

; FILING DATE: 24-JUN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Meilman, Edward A.

; REGISTRATION NUMBER: 24,735

; REFERENCE/DOCKET NUMBER: P/951-106

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 382-0700

; TELEFAX: (212) 382-0888

; TELEX: 236925

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1773 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

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; NAME/KEY: CDS

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; OTHER INFORMATION: /note= "Sucrose-Transporter"

US-08-356-340-3

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Db	365	GCGCGGACCTTGGTCAAGCTCCGGTGACAC-----TCTCGMAAAGGA	409
Qy	625	CTCGTTGGCACGCTGCGATCGTGTACGTTCTGGGTTTTGGTCTCTTGATCTTCTCCAAC	684
Db	410	TTTAAAGCACGCTGCCATTGCGGTTTTCGTCGTCGGCTTTTGGATCCCTTGATGTTGTAAAC	469
Qy	685	AACACTGTGCAGGGTCCAGCACGCTGTCATGCTGCTGCTATGTTGTGACCATCATG----	739
Db	470	AACATGTTACAGGGCCCATCGAGCACTACTGGCTGATCTCTCGCGGAAATACCGGC	529
Qy	740	-GGCCAAAGTCGGCTAACTCCATCTCTGTTCTTTGGATGCGGTGGGAAACATCTTAGGC	798
Db	530	AGGATGAGAACAGCAATGCTTTTCTCATCTTTCATGGCGCTCGGAAACATCTTGGGG	589
Qy	799	TACTCTCTCGCTCCACGAACATTGSCACAAGTGTGTTCCCTTCTTAAACAGAGCGCC	858
Db	590	TACGCCCGGTTCAATTTCTACCTCTTTAAGTATTCCTTTCTCAAAAACCAAGCC	649
Qy	859	TGCTGTGAGCCCTGTGCGAACCTGAAAGGTGCATTTCTGGTGGCCGFGTGTCTCTAGTC	918
Db	650	TGCGACATGTACTGCGCAATCTGAAGAGTTGTTTCTTCATCGCTATATTCTCTTTTACTC	709
Qy	919	CTGTGCTGACGTTAAACCTTGATCTTCGCAAGAGGTGCGTACAGAGCGA--ACGAG	975
Db	710	AGCTTAAACACCATAGCCTTAACTTAGTCCGGGAAACAGAGCTCCCGGAGAAAGACGAG	769
Qy	976	AACTCCCGACGACGAAGGCGCGCGGAGGTGAGACTGAGCTACTCCGGGCGCACTTGCC	1035
Db	770	CAAGAAATCGACGAGAAATTAGCGGCGCGGAAATCGAAAGTACCGTTTTTCGGTGAA	829
Qy	1036	GTGCTCAAGGGCTCAGGACCTGCTCCCGGATGCCGTCCGTCCTCGTACGACTGCC	1095
Db	830	ATTTTTCGGGCTTTGAAGAATAATACCTCGACCGATGFGAATCTCTATTAGTAACCTGT	889
Qy	1096	ATCACCTGGCTTTGCTGGTTCCCGTTTCATCCTCTACACACCGCACTGGATGGCGGGAG	1155
Db	890	TTGAATGGATCGCGTGGTTTCCCTTTTCTTATACGATACAGATTGATGGCTTAAGGAG	949
Qy	1156	ATCTACACCGGACCCCAAGGGAGCAACGCCACGATCTCGCGGTTCAACAGAGGTGTC	1215
Db	950	GTTTTCGGTGGACAAGTCCGTGTATGCGAG-----GTTGTACGATTTGGGGTGA	997
Qy	1216	CGAGTCGCGCGGTTTCGGGCTGCTACTCAACTCGGTTATTCTAGGGTTCAAGCTCGTTCCTG	1275
Db	998	CGGCTGCTGCATGGGATTAAGTTGTCATCTGTGTTCTAGGGTTATGTTACTTCTGGG	1057

## RESULT 4

US-08-786-555-3

: Sequence 3, Application US/08786555B

: Patent No. 5,981,181

; FACILE NO. 3901101  
: GENERAL INFORMATION.

; GENERAL INFORMATION: WOLF-BEYND

; APPLICANT: FROMMER, WOHL-BETHA  
APPLY TO: ADM DISCOURTIER TONG

APPLICANT: RIESMEIER, JORG

; TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE TRANSPORTER, OLIGOSACCHARIDE TRANSPORTER, AND OLIGOSACCHARIDE TRANSPORTER-ASSOCIATED PROTEIN

; TITLE OF INVENTION: PLASMIDS, BACTERIA AND PLANTS CONTAINING A TRANSPORTER

; TITLE OF INVENTION: AS WELL AS A PROCESS FOR PREPARATION AND

TITLE OF INVENTION: OF

FILE REFERENCE: Frommer

CURRENT APPLICATION NUMBER: US/

CURRENT AFFILIATION NUMBER: 00/00/00;  
CURRENT FILING DATE: 1997-01-21

CURRENT FILING DATE: 1997-01-21  
 ENTERED APPLICATION NUMBER: 08/

; EARLIER APPLICATION NUMBER: U8/356,340  
; PUBLISHED DATE: 1994-12-01

; EARLIER FILING DATE: 1994-12-21

; EARLIER APPLICATION NUMBER: PCT/EP93/01604

; EARLIER FILING DATE: 1993-06-22

; EARLIER APPLICATION NUMBER

: EARLIER FILING DATE: 1992-06

NUMBER OF SECTIONS TO BE SUBMITTED:

; NUMBER OF SEQ  
: COFTWAPF; Data

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; SOFTWARE: F
CFO ID NO 3

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; SEQ ID NO 3

; LENGTH: 1773

Overall Match	9 0%	Score	187	8:	DB 2:	Length	1773:
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<b>Query Match</b>	<b>Score</b>	<b>ID#</b>
Best match	98.8%	NC_056727
Next closest	98.0%	NC_056728

Best Local Similarity	48.8%	Pred: No. 9.3e-27	Indol	12.	Gang	6.

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QY 385 CTGGGCTTTACATCGCTCACTTCATCTGCTGCGGCTTATTCGCGCTTA 444  
 Db 185 CTCGGAATTCCTCAAAATTTGCTCTTTATTTGGCTTTTGGACCGAATTTCTGGTATG 244  
 QY 445 GTGGTCAAACCGCTGGTGGCTGTACAGCAGAGGTGTACATCGAGATGGGGAGAGCG 504  
 Db 245 ATTGTTACGCCAGTTGTGCGGTACTACAGTGATAATTTGCTCTCCGTTTGGTCCGCC 304  
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 Db 410 TTTAAGCCACGTGCCATTGCCGTTTTTGTGCTGCGTTTTTGGATCTCTGATGTTGCTAAC 469  
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 Db 470 ACATGTTACAGGCCCATGACAGCACTACTGGTGTATCTCTCGCGGAAATTCGCGC 529  
 QY 740 -GGCAAGTGGCTTAATCTCTGTTCTTGGATGGCGCTGGGAAACATCTAGGC 798  
 Db 530 AGGATGAGAACAGCAATTCCTTTTCTCATCTTTCATGGCGCTCGGAAACATCTGGGG 589  
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 QY 1690 GTGCTGGCGTGTTCCTGTGCTGCC 1712  
 Db 1478 GTTTTAGCACTCAATGTTGCC 1500

RESULT 5  
 US-08-486-049-1  
 ; Sequence 1, Application US/08486049  
 ; Patent No. 6572862  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Estes, Mary K  
 ; APPLICANT: Jiang, Xi  
 ; APPLICANT: Graham, David Y  
 ; TITLE OF INVENTION: Methods and Reagents to Detect and  
 ; TITLE OF INVENTION: Characterize No. 6572862walk and Related Viruses  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fulbright & Jaworski L.L.P.  
 ; STREET: 901 Pennsylvania Ave., N.W.  
 ; CITY: Washington, D.C.  
 ; STATE:  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/486,049  
 ; FILING DATE: June 7, 1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Davis, Peter  
 ; REGISTRATION NUMBER: 36,119  
 ; REFERENCE/DOCKET NUMBER: 311.023  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-662-0200  
 ; TELEFAX: 202-662-4643  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7724 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: cDNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: No. 6572862walk virus  
 ; STRAIN: 8FIIa  
 ; INDIVIDUAL ISOLATE: 8FIIa  
 ; IMMEDIATE SOURCE:  
 ; CLONE: pUCNV-953 and its derivatives  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 146..539  
 ; OTHER INFORMATION: /note= "The protein encoded by

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OTHER INFORMATION: nucleotides 146 through 5359 is eventually cleaved
OTHER INFORMATION: to make at least a picornavirus 2C-like protein, a
OTHER INFORMATION: 3C-like protease and an RNA-dependent RNA polymerase.
FEATURE:
NAME/KEY: CDS
LOCATION: 5346..6935
OTHER INFORMATION: /note= "Nucleotides 5346 through
OTHER INFORMATION: 5359 are used for coding two different amino acid
OTHER INFORMATION: sequences: the first is the sequence coded by
OTHER INFORMATION: nucleotides 146 through 5359, the second by nucleotides
OTHER INFORMATION: 5346 through 6935."

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CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA: US/09/095,443  
APPLICATION NUMBER: US/09/095,443  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/049,477  
FILING DATE: June 12, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 235/055  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4456 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-095-443-1

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid

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	Best Local Similarity	44.2%	Pred. No. 0.00012		
	Matches 381	Conservative	0	Mismatches 477	Indels 4
					Gaps 2
Qy	1231	GGGCTGCTACTCAACTCGGTATTCTAGGTTTCAGCTCGTTCGTATCGAGCCCATGTGC			1290
Db	178	GCGCCGCTGATCACGCGCGGAGCTGGGTCTGTCGTGTGTAACGCGCGGTGATCGCC			237
Qy	1291	CGGAAGGTGGGCGCGAGGGTGTGTGGTGCACGAGCAACTTCATGGTCTCGCTCGGCATG			1350



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; CURRENT APPLICATION NUMBER: US/09/554,337
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/065,791
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: PCT/CA98/01064
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: respiratory syncytial virus
US-09-554-337-4

Query Match          3.4%; Score 70.8; DB 4; Length 8100;
Best Local Similarity 67.8%; Pred. No. 0.00021;
Matches 99; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1943 CGATCAATCAATGTGTAGTAGTACAACTAGACGATGATGTCACATCATTTGCTTTTA 2002
Db      |||||
Qy 7859 CAATAATTGGAAGCTTACATAAGCTTAATTCGACGATAATTGGATTATTTTATTTT 7918
Db      |||||
Qy 2003 ATACATACCGGTTCTTATGTTCTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 2062
Db      |||||
Qy 7919 GCAATTGGTTTTTAATATTTCACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 7978
Db      |||||
Qy 2063 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2088
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Db      |||||

RESULT 15
US-07-920-281C-1
; Sequence 1, Application US/07920281C
; Patent No. 5739026
; GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik
; APPLICANT: Liljestrom, Peter
; TITLE OF INVENTION: DNA Expression Systems Based on
; TITLE OF INVENTION: Alphaviruses
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,281C
; FILING DATE: 13-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 828-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
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; ANTI-SENSE: NO
; ORIGINAL SOURCE: Semliki Forest Virus
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; NAME/KEY: -
; LOCATION: 1..11517 /label= genome
; OTHER INFORMATION: /note= "Semliki Forest Virus complete nucleotide
; OTHER INFORMATION: sequence, presented as a cloned DNA sequence; see
; OTHER INFORMATION: Figure 5."
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..7379
; OTHER INFORMATION: /product= "SFV polyprotein"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7421..11179
; OTHER INFORMATION: /product= "SFV polyprotein"
US-07-920-281C-1

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Best Local Similarity 67.8%; Pred. No. 0.00024;
Matches 99; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Db      |||||
Qy 11362 CAATAATTGGAAGCTTACATAAGCTTAATTCGACGATAATTGGATTATTTTATTTT 11421
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Qy 2003 ATACATACCGGTTCTTATGTTCTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 2062
Db      |||||
Qy 11422 GCAATTGGTTTTTAATATTTCACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 11481
Db      |||||
Qy 2063 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2088
Db      |||||
Qy 11482 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 11507
Db      |||||

Search completed: November 7, 2004, 14:41:40
Job time : 188 secs
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 09:12:46 ; Search time 1038 Seconds  
(without alignments)  
10830.476 Million cell updates/sec

Title: US-09-679-687b-1

Perfect score: 2088  
Sequence: 1 gcacgagacatcttcacact.....aaaaaaaaaaaaaaaaaaaaa 2088

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
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- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1557	74.6	1557	15	US-10-409-701-18
2	1472.8	70.5	1499	16	Sequence 18, Appl
3	1344.8	64.4	2248	18	Sequence 31902, A
4	1302.4	62.4	2470	17	Sequence 142617
5	1291.4	61.8	1372	16	Sequence 14354, A
6	1052.2	50.4	2223	15	Sequence 35042, A
7	1040.5	49.8	2092	15	Sequence 24, Appl
8	840.4	40.2	1600	15	Sequence 22, Appl
9	826.2	39.6	1831	15	Sequence 23, Appl
10	678.8	32.5	2235	18	Sequence 359, Appl
11	634.2	30.4	695	16	Sequence 4637, Ap
12	586.6	28.1	1910	16	Sequence 12513, A
					Sequence 4380, Ap

13	586.6	28.1	2262	18	US-10-425-115-120168	Sequence 120168,
14	543	26.0	1662	17	US-10-437-963-12595	Sequence 12595, A
15	531.8	25.5	1155	16	US-10-425-114-22383	Sequence 22383, A
16	330.8	15.8	1638	17	US-10-437-963-39173	Sequence 39173, A
17	330.4	15.8	2042	15	US-10-431-273-25	Sequence 25, Appl
18	328.2	15.7	1930	15	US-10-431-273-26	Sequence 26, Appl
19	327.2	15.7	1785	9	US-09-938-842A-1709	Sequence 1709, Ap
20	327.2	15.7	1785	11	US-09-938-842A-1709	Sequence 3, Appl
21	327.2	15.7	1785	13	US-10-247-813-3	Sequence 29, Appl
22	315	15.1	1818	15	US-10-247-813-29	Sequence 15792, A
23	310.8	14.9	2412	16	US-10-425-114-15792	Sequence 28392, A
24	310.8	14.9	2893	18	US-10-425-115-28392	Sequence 118588
25	305.4	14.6	1152	16	US-10-424-599-118588	Sequence 19222, A
26	281.8	13.5	1779	16	US-10-424-599-19222	Sequence 107947,
27	254.4	12.2	736	18	US-10-425-115-107947	Sequence 1316, Ap
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29	243	11.6	1539	11	US-09-938-842A-1316	Sequence 23, Appl
30	241.4	11.6	1539	17	US-10-318-390-23	Sequence 358, App
31	240.4	11.5	1680	15	US-10-310-154-358	Sequence 6426, Ap
32	236.8	11.3	2048	16	US-10-424-599-6426	Sequence 1624, Ap
33	229.8	11.0	1542	9	US-09-938-842A-1624	Sequence 1624, Ap
34	229.8	11.0	1542	11	US-09-938-842A-1624	Sequence 1624, Ap
35	229.4	11.0	1355	15	US-10-247-813-4	Sequence 1, Appl
36	225.6	10.8	1533	15	US-10-247-813-4	Sequence 57, Appl
37	225.6	10.8	2020	18	US-10-739-930-57	Sequence 35664, A
38	214.6	10.3	780	16	US-10-425-114-35664	Sequence 1525, Ap
39	214	10.2	572	17	US-10-021-323-1525	Sequence 2887, Ap
40	214	10.2	1310	17	US-10-767-795-2887	Sequence 25884, A
41	207.8	10.0	1844	16	US-10-425-114-25884	Sequence 25022, A
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ALIGNMENTS

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; Sequence 18, Application US/10409701  
; Publication No. US2003022124A1  
; GENERAL INFORMATION:  
; APPLICANT: Zinselmeyer, Chris  
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress  
; FILE REFERENCE: 1421  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,796  
; PRIOR FILING DATE: 2002-04-08  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 1557  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1557)  
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Best Local Similarity 100.0%; Pred. No. 0;  
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 QY 382 ACTCTGGGGTTTACATCGCTCACTTCATTTCATGTGGCTCTGCGGCCCTATTCCGGC 441  
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 QY 442 TTAGTGGTCCACCGCTGCTGGCTGTACACGACGAGTGTACATCGAGTGGGGAGA 501  
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 QY 562 TTCTCGTTCAGACATCGAGCTGCTTAGGGACACGAGGACACTGAGCCTTACAC 621  
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 QY 622 GGTCTCTGTGGCAGCTCGATCGGTGACGTTCTGGGGTTTGGCTCTTGAATTCCTC 681  
 Db 421 GGTCTCTGTGGCAGCTCGATCGGTGACGTTCTGGGGTTTGGCTCTTGAATTCCTC 480  
 QY 682 ACAAACACTGTGACGGTTCAGACGTCGTATGATGGCTGATCTATGTGACCATCGG 741  
 Db 481 ACAAACACTGTGACGGTTCAGACGTCGTATGATGGCTGATCTATGTGACCATCGG 540  
 QY 742 CCAAGTGGGCTAACTCCATCTCTCTGTTCTGGATGGGCTGGGAAACATCTAGGCTAC 801  
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 QY 802 TCTCTGGCTCCACGACAACTGGACAGTGGTTTCCCTTCTTAAACGAGGCGCTGC 861  
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 QY 862 TGTGAGGCTGTGCGGACCTGAAAGGTGCAATTTCTGTTGGGCGGTGGTCTTCTAGTCTC 921  
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 Db 721 TGCCTGACGTAACCTGATCTTCCGACGAGGTGCGGTACAGGAGGACGAGGACCTC 780  
 QY 982 CCGACGACGAGGCGGCGGAGGTGAGACTGAGCCTACCGGCGCACTTGCGTGCCTC 1041  
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 Db 1441 AACATCCCGGCTTTCGGGCTCGGCTTGCCTCTCGCGCGGCTGCTGGGCGTG 1500  
 QY 1702 TTCTCTGCTSCCAAGATCTCCAAAGCGCGCTTCGCGGCGCTCAGCGCGGCGCCAC 1758  
 Db 1501 TTCTCTGCTSCCAAGATCTCCAAAGCGCGCTTCGCGGCGCTCAGCGCGGCGCCAC 1557

RESULT 2  
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 ; Sequence 31902, Application US/10425114  
 ; Publication No. US2004003488A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(5313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 31902  
 ; LENGTH: 1499  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: UC-ZMFLB73232A01\_FLI  
 US-10-425-114-31902

Query Match 70.5%; Score 1472.8; DB 16; Length 1499;  
 Best Local Similarity 99.5%; Pred. No. 3.1e-311;  
 Matches 1488; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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 QY 594 CACGAAAGAACATGACGCTCTACCAACGCTCTGTTGGCAGGCTGCGATCGTGTACGT 653  
 Db 63 CACGAAAGAACATGACGCTCTACCAACGCTCTGTTGGCAGGCTGCGATCGTGTACGT 122  
 QY 654 TCTGGGTTTTGGCTCTTCTGACTTCTCCAAACACATGTGCGAGGTCACAGACGTGCTAT 713  
 Db 123 TCTGGGTTTTGGCTCTTCTGACTTCTCCAAACACATGTGCGAGGTCACAGACGTGCTAT 182  
 QY 714 GATGCTGATCTATGTGACCATCATGGGCGAAGTGGGCTAACTCATCTTCTGTTCTTG 773  
 Db 183 GATGCTGATCTATGTGACCATCATGGGCGAAGTGGGCTAACTCATCTTCTGTTCTTG 242  
 QY 774 GATGCTGCGGAAACATCTAGGCTACTCTCTGCTCCAGGAAATTTGGCAACAAGTG 833  
 Db 243 GATGCTGCGGAAACATCTAGGCTACTCTCTGCTCCAGGAAATTTGGCAACAAGTG 302





Qy	789	CATCTAGGCTACTCTCTGGTCTCAGAACAATGGCAGAAGTGGTTCCCTTCCTTAA	848
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Qy	849	AACGAGCCCTCTGTGAGGCTGTGCAACTCAAAAGTGCAATTTCTGGTGGCCGNGT	908
Db	1010	AACAAATGCTTGTGAAGCTGTGCAAACTGAAGTGCAATTTCTGGTGGCTGGT	1069
Qy	909	GTTCTAGTCTGTGCCGTGACGGTAAACCTGATCTTCCCAAGAGGTGCGTACAGAGC	968
Db	1070	GTTCTAGTCAATAGTTGGTATAAACCTCGTCTTGCCCAAGAAAGTACCATACAGG	1129
Qy	969	GAACGAGAACTCCCGACGACGAAGGCGCGGCGAGCTCAGACTCAGCTACCGGGCC	1028
Db	1130	AAACGAGAACCTCC--CAACAAAGCAAAACGGCGAGGTGAAGCTGAACTACCGGGCC	1186
Qy	1029	ACTTGGCTGCTCAAGGCTTCAAGACCTGCTCCCGGATGCCGTGCTGCTCTCGT	1088
Db	1187	ACTTGGTGTCTCAAGGCTTCAAGAACTTSCCCCGGGATGSCATCCGTTCTTCTCGT	1246
Qy	1089	GACTGCCATCACCTGGCTTTCGTGGTTCCCGTTCACTCTTACGACACGACTGGATGGG	1148
Db	1247	AACTGGCTCACTGGCTCTGTGGTTCCCGTTCACTCTCTACGACACCGACTGGATGGG	1306
Qy	1149	CCGGAGATCTACACGGCGACCCCAAGGGAGCAACGCCAGATTCGGCGTTCAACGA	1208
Db	1307	CCGTGAGATCTACACGGCGACCCCAAGGGACCAATGCTCAGATCTCGGCATTCACGA	1366
Qy	1209	AGTGTCCGAGTCCGGCGGTTTCGGGCTGCTACTCAACTCGGTTATTTCTAGGTTCACTC	1268
Db	1367	AGTGTGAGAATAGGCGATTCGGGCTGCTTCTCAACTCGATTTCTAGATTCAGTCTC	1426
Qy	1269	GTTCTGATCGAGCCCATGTGCCGAAGTTCGGGCCGAGGGTGGTGGTGACAGCAA	1328
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Qy	1329	CTTCAATGTTCTGCTCGCATTGGCGGCCACCGCGCTCATCAGCTTCTGTGCTCAGGGA	1388
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Qy	1389	CTACACGGGTAAGTGACGAGACGCATCAACGGAAACGCCAGCATCAAGGCCGTTCTGCCT	1448
Db	1547	CTACACGGGTAAGTGACGAGACGCATCAACGGCAGACGAGCATCAAGGCCGTTCTGCCT	1506
Qy	1449	CGTCTCTTTCGCTTCTGCGGCTCTCTCGCCATCTCTGACAGTCCCGGTTCCGCT	1508
Db	1607	CGTCTCTTTCGCTTCTGCGGTTCTCTCTCGCATCTCTGACAGTCCCGGTTCCGCT	1566
Qy	1509	GACGGCCAGTGGCGGCCACCGCGGCGCGGGCAGGGCTGTGCAACCGGCTCTCTCAA	1568
Db	1567	GACGGCCAGTGGCGGCCACGATGGCGGCGGGCAGGGCTGTGCAACCGGCTCTCTCAA	1726
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Qy	1629	GTTCCGGAAGGCAACATCCCGGTTTCGGCTGCGGTTCGGCTTCGCCCTCTCGCGCG	1688
Db	1787	GTTCCGGAAGGCAACATCCCGGTTTCGGCTGCGGTTCGGCTTCGCCCTCTCGCGCG	1846
Qy	1689	CGTCTGGGCGTGTCTGTGCCAAGATCTCCAAGCGCACTTCGGGCGCTCAGCGC	1748
Db	1847	CGTCTGGGCAATGTTCTGTGCCAGATCTCCAAGCGCACTTCAGGCGCTCAGCGC	1906
Qy	1749	GGGCGGCACTGATCGAAACCGCGCGGGCGCGCG	1784
Db	1907	GGGCGGCACTGATCGAGCACGGCCCGCGCGCGG	1942

## RESULT 5

US-10-425-114-35042

00-10-423-111-35042 ; Sequence 35042, Application US/10425114

; Publication No. US20040034888A1





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1306	DB	CTGATCAGAGCCGATGTCAAGCGGCTAGGCCGAGGGTGTTGGGTGTTCCAGCAATTC	1365
1333	QY	ATGGTCTTCGCTCGCCATGCGGGCCACCGCGCTGATCAGCTTCTGGTTCGCTCAGGGACTAC	1392
1366	DB	CTCGTCTGCAATCGTATGGCTGCGCACCGCCATCATCAGCTGGTGGTCTACCAAGGAATTC	1425
1393	QY	CACGGGTACTGTCAGAGACGCCATCAACGGGAAACGCCAGATCAAGGCCGCTCTGCCTCGTC	1452
1426	DB	CATGAGTACGTTGAGCATGGCATTACCGCCAGCAAGGACATCAAAATCGTATGCATGGCC	1485
1453	QY	CTCTTTGGCCCTTCTGGCGGTCCTCTCGCCATCTGTACAGCGTCCCGTTTCGGGTGACG	1512
1486	DB	CTCTTTCGCAATCTCGGAGTGCCTCTCGCCATTCTGTACACGGTTCCTTTTCGGGTGACG	1545
1513	QY	GCCAGCTGCGGCGCACCCGGGGGGGGGCGAGGGGTGTGCAACGGCGTCTCTCAACATC	1572
1546	DB	GCGCAGTTGCGGCAAGCAAGGAGGGCGGCAAGGGCTGTGTCAACCGCGTGTCTGAATATC	1605
1573	QY	TCCATCGTCAATCCTCAGGTGATCATCGCGCTGGGGCCGGCCGCTGGGACGCGCTGTTC	1632
1606	DB	TCCATCGTCAATCCCAAGGTGATCATCGCGCTGGGGCGGGGCGTGGGACCAAGCTGTTTC	1665
1633	QY	GGGAAGGCAACATCCCGCGCTTGGCGGTCCGCTCGGCCCTTCGCCCTCTGTCGGCGGCTC	1692
1666	DB	GGGAAGGCAACATCCCGCGCTTGGCGCGGCCCTTCGCCCTTCGCGCTCATTCGGCGGCAATC	1725
1693	QY	GTGGGGGTGTTCTGTGTGCCCAAGATCTCAAGCGCAGTTCGGGGCCGTCAGCGGGGC	1752
1726	DB	GTCCGCAATATCTGTGTGCCCAAGATCTCAGGCGCTCTGTTTCGGGCCGTCAGCACCGGC	1785
1753	QY	GGCACTGATTCGAACCCCGCGGGCGGGCCGCCGCAACGACCCCG	1799
1786	DB	GTCATGACCGCGTTCGGGGCGCTGCTGAGCGCGGCGAAGCTCG	1832

RESULT 8  
IIS-10-431-273-23

US-10-431-273-23  
; Sequence 23, Application US/10431273

Sequence 23, Application US/104  
; Publication No. US20030237108A1

; GENERAL INFORMATION:

; APPLICANT: Demmer, Jeroen

APPLICANT: Shenk, Michael

; APPLICANT: Glenn, Matthew

REFUGANT: GREENI, MACCIE  
APPLICANT: NO. US20030237

APPLICANT: Saulsbury, Keith

APPLICANT: Hall, Claire

; AFFILIANT: Hall, Claire  
; APPLICANT: Forster, Richard

; AFFILIANT: FOISLER, RICHARD  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF HIV-1 INFECTION

;	TITLE OF INVENTION:	COMPOSED BY:
;	TITLE OF INVENTION:	COMPOSED BY:
;	TITLE OF INVENTION:	COMPOSED BY:

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; TITLE OF INVENTION: GLASS
;
; FILE REFERENCE: 11000.10699

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; FILE REFERENCE: I1000.I083
; CURRENT APPLICATION NUMBER

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: CURRENT APPLICATION NUMBER  
:  
: CURRENT FILING DATE: 2003

;; CURRENT FILING DATE: 2005  
;; NUMBER OF SEO ID NOS: 92

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; NUMBER OF SEQ ID NOS: 92
: SOFTWARE: FastSEO for Wind

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; SOFTWARE: FASTSEQ FOR WIND
; SEO ID NO 23

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; SEQ ID NO 23
;      LENGTH: 1600

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; LENGTH: 1600
; TYPE: DNA

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; TYPE: DNA  
; ORGANISM: Festuca arundinacea

US-10-431-273-23

US-10-431-273-23

Query Match	40
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Query Match	40.
Best Local Similarity	79

Best Local Similarity 79:  
Matches 1007: Conservative

Matches 100%; Conservative

534 CATCTGCGTTGCCCGCT

QY 534 CATCTGCGTTGCCGT

2 CATCGCGTTCCTCT

**D<sub>b</sub>** 2 CATCTGCGTTGCTGT

EQ4 CACGACGACACCTC

QY 594 CACGAAGGAACACTG

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Db 62 TAGCAAGGAAGAGTG

Qy	654	TCTGGGTTTTCGTCTCCTCACTTCTCCAAACAACATGTGCAGGGTCAGCACGTGCTAT	713
Db	122	GCTTGGAATTCTGGCTTCTTCACTTCTCCAACAATCTGTCCAAGGTCAGCTCGTGCTCT	181
Qy	714	GATGGCTGATCTATGTGACCATCATGSGGCCAAGTGGCGCTAACCTCATCTCTGTTCTTTG	773
Db	182	GATGGCTGATTTGTTCAGGCAAGTATGACCCAGTGTGCMAATTCAATCTTCTGTTCTTG	241
Qy	774	GATGGCGCTGGGAAAACATCCTTAGGCTACTCTCTGCTCCACGAAACAATTTGGCACAAGTG	833
Db	242	GATGGCGCTAGGAAAATATCCTAGGTAATCTCTAGGTAATCTCTCTGGTTCCACAGATAAGTGGCACAAGTG	301
Qy	834	GTITTCCTTCTTAAACAGAGCGCTCTGTGAGGCTGTGCAGAACTCGAAAGGTGCATT	893
Db	302	GTITTCCTTCTTTCGGCAAGAGCGCTGTGTAGGCTTTGGCAAATTTGAAGGCGCTTT	361
Qy	894	TCTGGTGGCCGTGGTGTTCCTAGTCTCTGTGCCTTGAAGGTAAACCTCATCTTCGCCAAGA	953
Db	362	TCCTGGTGCTGTCTGTCTGTGCTTCTGTTTTGGTATAAATCTGATCTTGCCCAAGA	421
Qy	954	GTGTCCGTACAGAGCGAAACAGAAACCTCCGACGACGAAAGCCGCGGAGGTCCAGAC	1013
Db	422	GGTACCATAAACAAGAAATGACCCCTCC---CAACAAGGCCAAATTTGGTCTGAAGT	478
Qy	1014	TGAGCTTACCGGGCCACTTGGCGTGCTCAAGGCTTCAAGGACCTGCCTCCGCGGATGCG	1073
Db	479	TGAACCTAGTGGCCGCTTGGCGTGTCCAGGCTTCAGAACTTGCCTTCGGAAATGCC	538
Qy	1074	GTCCGTGCTCCTCGTGAATGCCATCACTGGCTTTCGTGGTTCCCGTTCACTCTCTACGA	1133
Db	539	ATCGTGCTCTTTGTAATGGCTCACTTGGCTTCTCTGGTCTCTGGTCTCCGTTCACTCTCTACGA	598
Qy	1134	CACGACTGATGGCGGGAGATCTTACCACGCGACCCCAGGGGAGCAAGCCCGAGAT	1193
Db	599	CACCGACTGATGGGTCTGTGAGATTACCACGCTGACCCCAAGGGCACCCAGCTGAGCG	658
Qy	1194	CTCGGGCTTCAAACGAAGTGTCCGAGTCCGGCGGTTTCGGGCTGTCTACTCAACTCGGTTAT	1253
Db	659	CTCGGCTTCCAGACGGTGTCAAGGCTGGCGGTTTCGGACTGTACTCAACTCGATCAT	718
Qy	1254	TCTAGGGTTCAGCTCGTTCTGTATCAGCGCATGTGCCGGAAGTTCGGCGCAGGGTGT	1313
Db	719	CCTGGGGTTCAGCTCGTTCTGTATCAGCGCATGTGCAAGCGGCTGGGCGCGAGGGTGT	778
Qy	1314	GTGGGTGACGAGCAACTTATGGTCTGCGTTCGCATGCGGGCCACCGCGCTCATACGCTT	1373
Db	779	GTGGGTGTCCAGCAACTCTCTGTCTGCATGCGCATGGCGCCACCGCCATCATCAGCTG	838
Qy	1374	CTGGTCTCAGGGAATCAACAGGGTACGTGCAGGACGCCATCACCGGAAACGCCAGCAT	1433
Db	839	GTGGTCTACCAAGAAATTCATGAGTACGTCCAGCATGCCATCACCGCCAGCAAGACAT	898
Qy	1434	CAAGGCGCTGCTGCTCTCTCTCTTCCTTCCTGGCGCTCCCTCTCGCCATCTCTGTACAG	1493
Db	899	CAAGATCGATGATGGTCTCTTTCGCATTCCTTCGAGTGCCTCTCGCCATCTGTACAG	958
Qy	1494	CGTCCGTTTCGGTGAACCGCGCATGTGGCGCACCCCGGGCGGGCGAGGGCTGTG	1553
Db	959	CGTTCCTTTCGGTTCACGCGCAGTGTGGCGGCAACAAGAGAGGGCGGCAAGGGCTGTG	1018
Qy	1554	CACGGCGTCTCAACATCTCATCTGTATCTCCTCAGGTGATCATCGCTCGGCGCGCGG	1613
Db	1019	CACGGCGTGTGAAATCTCATCTGTATTCATCCACAGGTGATCATCGCGCTGGGGCGGG	1078
Qy	1614	CCGTGGGACGCGCTGTTCGGGAAGGGCAACATCCCGGCGTTTCGGCGTCCGCTCGGCTT	1673
Db	1079	GCGTGGGACCACTGTTCGGGAAGGGCAACATCCCGGCTTTCGCGCGCGCTTCGCGCTT	1138
Qy	1674	GCGCTCTGTTCGGCGGCTGTGGGCGTGTCTGTGTGCCAAGATCTCCAAAGGCGAGTT	1733
Db	1139	CGCGCTCATCGGCGGCATGTCGGGCATATTCCTGTGTGCCAAGATCTCCAGGCACTCGTT	1198



QY 1734 CCGGGCCGTACGCGGGGGCCCACTGATCGAACCGCGCGGGCCGCCCGGCACGC 1793  
 Db 1199 CCGGGCCGTACGCGGGGGCCCACTGATCGAACCGCGCGGGCCGCCCGGCACGC 1258  
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 Db 1259 AGCTCG 1264

RESULT 9

US-10-310-154-359  
 ; Sequence 359, Application US/10310154  
 ; Publication No. US20030233670A1  
 ; GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D  
 APPLICANT: Chomet, Paul S.  
 APPLICANT: Adams, Thomas H.  
 APPLICANT: Ruff, Thomas G.  
 APPLICANT: Agarwal, Ameeta K.  
 APPLICANT: Ahrens, Jeffrey E.  
 APPLICANT: Ball, James A.  
 APPLICANT: Banu, G.  
 APPLICANT: Bell, Erin  
 APPLICANT: Boddupalli, Raghava  
 APPLICANT: Deikman, Jill  
 APPLICANT: Deng, Molian  
 APPLICANT: Dong, Jinzhao  
 APPLICANT: Duff, Stephen M.  
 APPLICANT: Galligan, Meghan M.  
 APPLICANT: Hinchey, Brenda S.  
 APPLICANT: Huang, Shinsieh  
 APPLICANT: Johnson, G. Richard  
 APPLICANT: Jung, Vincent  
 APPLICANT: Kretzmer, Keith A.  
 APPLICANT: Laccetti, Lucille B.  
 APPLICANT: Lee, Gary  
 APPLICANT: Lin, Jie-yi  
 APPLICANT: Liu, Jingdong  
 APPLICANT: Lu, Bin  
 APPLICANT: Luethy, Michael M.  
 APPLICANT: Lund, Adrian  
 APPLICANT: Madson, Linda L.  
 APPLICANT: Malloy, Kathleen A.  
 APPLICANT: McKiel, Christine L.  
 APPLICANT: Miller, Philip W.  
 APPLICANT: Padmavathi, Manchikanti  
 APPLICANT: Parnell, Laurence D.  
 APPLICANT: Start, William G.  
 APPLICANT: Tennesen, Dan  
 APPLICANT: Vidya, K.R.  
 APPLICANT: Wang, Haiyun  
 APPLICANT: Xin, Zhanguo  
 APPLICANT: Xu, Nanfei  
 APPLICANT: Yang, Chunzhi  
 APPLICANT: Zeng, Xiaoping  
 APPLICANT: Zhang, Qiang  
 APPLICANT: Zhao, Rajuan  
 APPLICANT: Zhou, Li  
 TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants  
 FILE REFERENCE: 38-15(52796)B  
 CURRENT APPLICATION NUMBER: US/10/310,154  
 CURRENT FILING DATE: 2002-12-04  
 PRIOR APPLICATION NUMBER: 60/337,358  
 PRIOR FILING DATE: 2001-12-04  
 NUMBER OF SEQ ID NOS: 736  
 SEQ ID NO 359  
 LENGTH: 1831  
 TYPE: DNA  
 ORGANISM: Zea mays  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (76)..(1599)

OTHER INFORMATION:  
 US-10-310-154-359  
 Query Match 39.6%; Score 826.2; DB 15; Length 1831;  
 Best Local Similarity 72.5%; Pred. No. 4.2e-170;  
 Matches 1090; Conservative 0; Mismatches 398; Indels 15; Gaps 1;  
 QY 252 CCGCGGGCCGTGTTGGACCCACCGTGGCGCCGAGTACAGCTCGGAGGCTCATCTCGC 311  
 Db 105 CAGCGGGGTGGCGCGGCAAGAGCCGAGATCAGCCTTTTGGGGTGTTCCTCGC 164  
 QY 312 CGGCATGGTCGCGGGGGCGTGCAGTACGGCTGGGGCTGCAGCTCTCCCTCCCTCAGCC 371  
 Db 165 CTGCATGGTCGCGGGGGCGTGCAGTACGGATGGCGCTGCAGCTCTCCCTCTCAGCC 224  
 QY 372 CTAGTCAGACTCTGGGGCTTTTCAATGCGCTCACTTCAATTCATGTTGGTCTCGGCC 431  
 Db 225 CTAGTCCAGACACTGGGATTCCTCATGCTCTTATCATCATGTCATGTCGTGGAC 284  
 QY 432 TATTGCGGCTTAGTGGTCCAAAGCGCTGGTGGCCCTGTACAGCGACAGGTGTACATCGAG 491  
 Db 285 TATTGCTGGCTTACTTGTACAAACCTCGCTCGGCTCTATAGTACAAATGCATCTTAA 344  
 QY 492 ATGGGGAGACGGAGCGCTTTATCTGACAGGGTGCATGCTCATCTCGGTTCCCGTCAT 551  
 Db 345 GCTTGGAGACGGAGGCCATTTCATCTTTACAGGATGCATCATCTGTATATCTGTGAT 404  
 QY 552 TGTGTGCGGATTCCTGTCAGACATCGAGTGTCTTAGGGGACACGAAGAACTGCAG 611  
 Db 405 AGTCATCGGTTTCTCTCAGACATCGGTACGCTCTCGGTGACACGACGGAAGACTGCAA 464  
 QY 612 CCTTACACGGTCTCTGTTGGCACTGCGATCGTGTAGTCTCTGGGTTTGGTCTCT 671  
 Db 465 TGTTCACCGGGAAGCGGCTGCACGCGCTTGTCTTCTGATGGGATCTGGTGTCT 524  
 QY 672 TGACTTCTCCAAACACACTGTGCGAGGTCCAGACGCTGATGATGCTGCTATGATGTA 731  
 Db 525 GGACTTTTCCAAACACACGCTGCGAGGCCCCCGACGCGCTGATGGCGACCTCGCAGG 584  
 QY 732 CCATCATGGCCCAAGTGGGCTAACTCCATCTTCTGTCTTGTGATGGCGTGGGAAACAT 791  
 Db 585 CAGCCACGGACCCAGACGCGGAAACGCACTCTTCTGTGCTGTGATGGCGTGGGAAACAT 644  
 QY 792 CTTAGGCTACTCTCTGGCTCCAGCAACAATGGGCAAGTGGTTCCTTCTTAAAC 851  
 Db 645 CTTGGGCTACTCTCTGGGTTCCACGACAGTGGGCACTGTTTCCCGTCTCTGCGAGC 704  
 QY 852 GAGCGCTGCTGTGAGGCTGTGCGAACCTGAAAGGTGCACTTCTGTGGCCCTGGTGT 911  
 Db 705 GAGGGCATGTGCGAGCGTGGCGCACTCAAGGCGGCTTCTGGTGTGGTGTGT 764  
 QY 912 CTTAGTCTGTGCTGACGGTAAACCTGTATCTTTCGCAAGAGGAGGTGCGGTACAGAGCAA 971  
 Db 765 CTTGGGCTGTCCACGCTGGTGGTACCATGATCTTTCGCGCGAGGTGCTTCTGGGCTGT 812  
 QY 972 CGAAGACCTCCGACGACGAGGCGCGGCGGAGGTGAGACTGAGCTTACCGGCGCACT 1031  
 Db 813 ---GCTGGACCCGCGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 869  
 QY 1032 TGGCGTCTCAAGGGCTTCAAGGACCTGCTCCCGGGATGCCCTGCTGCTCTCGTGAC 1091  
 Db 870 CGCGGTTTTCAAGGGCATGAAGAAACATGCCCGCGCATGCCGAGGTGCTCATCGTCAC 959  
 QY 1092 TGGCATCAGCTGGCTTTCGGTTCGGTTCATCTCTAGCACCGACTGGATGGCGCG 1151  
 Db 930 GGGCCTCAGCTGGCTCTCTGGTTCGGTTCATCTCTTTCGACACCGACTGGATGGCGCG 989  
 QY 1152 GGAGATCTACACGGGACCCCAAGGGGAGCAACGCGCCAGATCTCGCGCTTCAACGAAG 1211  
 Db 990 CGAGATGTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1049  
 QY 1212 TGTCCGAGTGGCGGCTTGGGCTGCTACTCACTCGGTTATTTCTAGGTTTACGTCGTT 1271







Qy	936	CTTGATCTTTCGCGAAGAGGTTGCGGTACAGAGCGAA	CGAGAACTCTCCGACGACGAAGGC	995
Db	974	CTTGTGGCTCGCGCGAGGAGCGG-----CTCGAC	AGGAAG	1012
Qy	996	CGGGCGGAGGTCGAGACTGAGCCTACCGGGCCACTT	GCCTGCGTCAAGGCTTCAAGGA	1055
Db	1013	CGTCGACACCTCGGCGCGGCTCTCGCGTTCATG	ATCTCTTCAAGACCTCAGAA	1072
Qy	1056	CTGCTCCCGGATGCGGTCCGTCTCTGCTGACTG	CGCATACTGTGGCTTCTGCTGGTT	1115
Db	1073	GCTTCGCGCTCCCATGTTACGCTGCTCGCGT	CACGCCGCTCATGTGCTCTGCTGGTT	1132
Qy	1116	CCCGTTCACTCTTACGACACCGACTGGATGGG	CGGCGAGATCTACACGCGACCCCAA	1175
Db	1133	CCCCCTCTTCCAGTACACACCGACTGGATGGG	CGGCGAGATCTTCCACGGCGAGCCGA	1192
Qy	1176	GGGAGACACGCCCGAGATCTCGGCGTTCAACGA	AGGTGTCCGAGTCTGGCGGCTTTCGGGCT	1235
Db	1193	GGGCGCGCGCGGAAAGGCGGACCTGTACGA	AGCGCGGTCCGCGAGGCGCCATTCGGCCT	1252
Qy	1236	GCTACTCAACTCGGTATTCTAGGTTACAGTTC	AGTCTGCTGATCGAGCCCATGTGCCGAA	1295
Db	1253	CCATTCTGCTCGTTCGGCTCGGTGTACCTCTT	CTTCAI CCCAGGCTGTGCCGAA	1312
Qy	1296	GGTCGGCCGAGGTGGTGTGGGTGACGAGCAACT	TTCATGCTTCGCTGCCTATGCGCATGCGCGC	1355
Db	1313	GCTCACGTCCCGGTCGTCTGTCGTCCGTCAG	CAGCCTGATGGTGTCTCTCATGACGCG	1372
Qy	1356	CACCGCTGATCAGCTCTGGTCGCTCAGGACTAC	ACCGGTACGTGCAGAGCGCAT	1415
Db	1373	CATGGTCGTCTCGCATGTTCTCCATGAAGGGT	TACAGGCCCTCGCTTCGCGGCTCTCT	1432
Qy	1416	CACCGCAACCCAGCA---TCAAGGCGGTTCGCT	CGTCTCTCTTCCTCCCTTCCTGGCGGT	1472
Db	1433	CTCTGGCCCCGACCACTCGTTTCAAGGGCGGG	CGCCCTCGCCATCTTCGCGTCTATCGSCAT	1492
Qy	1473	CCCTCTCGCATCTGTACAGCTCCGCTTCGCGGT	TGACGCGCAGCTGGGCGCACCG	1532
Db	1493	CCCTCAGGCGGTCTCTACAGGTGCTTGGGCGGT	TGGCGGTTCGAGGTGCCACCGAGGA	1552
Qy	1533	GGGCGGGCGGAGGGGTGTGCACCGCGTCTCAAC	ATCTCCATCTCATCTCCCTCAGGT	1592
Db	1553	CGGCGGTGTTCAAGTCTCACATTGGCGTCTTCA	ACATTGCAATCTCTCTTCCACAGCT	1612
Qy	1593	GATCATCGCGTGGGCGCGCCCGTGGGAGCGCCT	GTTCGGHAGGGCAACATCCCGGC	1652
Db	1613	GGTGATCGCGTGGGCGAGGCCCATCGACGGCG	CCCTTCAACAAGAGGAACACCCCGGC	1672
Qy	1653	GTTCCGGGTTCGCTTCGCGCTTCGCGCGCGGT	CTGCGGCGGTCTGGTGTCTGCTGCC	1712
Db	1673	CTTCGGCATCGGCGCGCTTCGCGCTTATCTG	CGCGGTCTCTGGCGTCACTCTCTCCC	1732
Qy	1713	CAAGATCTCCMAGCCGAGTTCCGGGCGGTTCAG	CGGGCGGCACATGATCGA	1765
Db	1733	AAAGCAGAGAGCGCTCTCCAACGCCACCGTCA	TGCGCGGGGCACTGATCTA	1785

RESULT 14  
US-10-437-963-12595  
; Sequence 12595, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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, FILE REFERENCE: 38-21(53221)B
, CURRENT APPLICATION NUMBER: US/10/437,963
, CURRENT FILING DATE: 2003-05-14
, NUMBER OF SEQ ID NOS: 204966
, SEQ ID NO 12595
, LENGTH: 1562
, TYPE: DNA
, ORGANISM: Oryza sativa
, FEATURE:
, OTHER INFORMATION: Clone ID: PAT_MRT4530_18708C.1
US-10-437-963-12595

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Query Match	26.0%	Score 543	DB 17	Length 1662
Best Local Similarity	62.6%	Pred. No. 2.5e-108		
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	Gaps	4		
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Db	148	AGGATCGTGGCTGTCTTCGCTGCATGGTGGCGCGCATCCAGTACGGCTGGCG	207	
Qy	349	CTGAGCTCTCCCTCTCTCAACGCGCTACGTGCAGACTCTGGGGCTTTCACATGGCGCTCACT	408	
Db	208	CTGAGCTGTCCCTCTCTCTCGCTACTCTTCAGACTCTCGGGATTTCCCACTCGTACGTT	267	
Qy	409	TCATTCATGTGGCTCTGCGGCCCTATTTCGCGGCTTAGTGTGCAACGCTGGTTGGCGCTG	468	
Db	268	TCCCTGACATGGATCTCGGAGCAATCGCTGGATTTGTGTGCAACCATCTGCTGGTTAC	327	
Qy	469	TACAGGACAGGTGTATCATCGATGGGGAGACGGAGCGGCTTTATPCCTGACAGGGTGC	528	
Db	328	TACAGTGACAGATGACCATGAAGTGGGCGCGAGGAGGCTTTCATCCTTTGTGGCTGC	387	
Qy	529	ATGCTCATCTCGCTTGGCGCTCATGTGTGCGGATCTTCGTCAGACATCGGAGTGTCTTA	588	
Db	388	CTCATCATCTGCAATCTCGTCATGATCATCGGTTTCTCGGCGGACATGACGTCACCTC	447	
Qy	589	GGGACACAGGAACAACCTCAGCCCTCTACACGGTCTCTGTTGGACGGTGGGATCGTG	648	
Db	448	GGTGACACCAAGACACTGCAGCACGTACACGGTCTCGCTGGTGGCGCGCATGGTG	507	
Qy	649	TAGTTCTGGGTTTGGCTTCTTGACTTCTCCAAACAACACTGTGAGGGTTCAGACAGT	708	
Db	508	TACATTGTTGGCTTCGTGTTCTTGACTTCGCTTAAACAACACTGTCCAGGGCGGCTCGT	567	
Qy	709	GCTATGATGGCTGATCT---ATGTGACCATCATCGGCGCAAGTCGGGTAACCTCATCTTC	765	
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Qy	766	TGTTCTTGGATGGCGTGGGAAACATCTTAGGCTACTCTCTGTGCTCCACGAAACAATGG	825	
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Qy	826	CACAAG-----	831	
Db	688	CACGACATTTGTCGGTGTGGCTAACTATGGTGTTCGTTGATCGCGGCATTCGTCAGA	747	
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Qy	1012	ACTGAGCCTACGGGCCACTTGGCGTGCTCAAGGCTTCAAGGACCTGCTCCCGGGATG	1071	
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Qy	1072	CCGTCCGTGCTCCTCGTACTGTCATCACTGCGCTTTCTGTGGTTCCGGTTTCATCCTCTAC	1131	

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Db 970 TTCAAAGTCTCGCGTACAGCGCGTCACTGGTGTGTGTTTCCCTTTCATCCAGTAC 1029
QY 1132 GACACCGACTGGAGCGCGGAGATCTACACGCGGACCCCAAGGGAGCAAGCCCGAG 1191
Db 1030 AACACCGACTGGAGCGCGGAGATCTACACGCGGAGCGCGGAGCGGAGCGGAGCGG 1089
QY 1192 ATCTCGGCTTCAACGAAGGTTCGAGTCCGCGCGTTCGGGCTGCTACTCAATCGGTT 1251
Db 1090 GCGACGCTGACAGCGCGCGTCAAGGAGCGCGCATGGGCTGCTTCTGCTCGCTC 1149
QY 1252 ATCTAGGCTTCAAGTCTGATCGAGCCATGTGCGGAGGTTCGGGCGGAGGCGG 1311
Db 1150 GCGCTCGGCGTCACTCTCTGATATCCCAAGCTCTGCGGAGCTGAGTCCAGGTTG 1209
QY 1312 GTGTGGGTGACGAGCAACTTCATGCTGTGCTGCTGCGGCGGAGCGGCGGCTGATCAGC 1371
Db 1210 GTCTGGTCCATCAGCAACTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1269
QY 1372 TTCTGGTCTGAGGACTACCAAGGTACGTGAGGAGCGGAGCGGCGGCGGCGGCGG 1428
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QY 1669 GCTTCTGCGCTGCTGCGGCGGCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1728
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QY 1729 CAGTTCGCGGCGGCTGCGGCGGCGGCGGCGGCT 1759
Db 1630 TCCACGCGCGGCTGCTGCTGCGGCGGCTCACT 1660
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## RESULT 15

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US-10-425-114-22383
; Sequence 22383, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22383
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Oryza sativa nipponbare
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3479-003-F5_FLI
US-10-425-114-22383
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Query Match 25.5%; Score 531.8; DB 16; Length 1155;
Best Local Similarity 80.4%; Pred. No. 6e-106;
Matches 623; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
QY 981 CCCGACGACGAAGCGCGGCGGAGTCTGAGACTGAGCTTACCGGGCCACTTGGCGTCT 1040
Db 26 CTTCCCAACAATAATCAACGAGCCAGCTGAGCTGAGGCACTGGTCCACTAGCAGTGT 85
QY 1041 CAAGGCTTCAAGGACCTGCTCCCGGATGCGTCCGTGCTGCTGCTGCTGCTGCTGCTG 1100
Db 86 GAAAGGCTTCAGAACTTACCTACTCTGAGGATGCTTCTGCTGCTTATGCTGCTGCTTAC 145
QY 1101 CTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1160
Db 146 CTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205
QY 1161 CCACGCGACCCCAAGGGGAGCAACGCCAGATCTGCGGCTTCAACGAAGGTGCCAGT 1220
Db 206 CCACGCTGACCCCAAGGAACTGATCTCAGATCAGGCTTCAACCAAGGCTGTCAGGCG 265
QY 1221 CGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1280
Db 266 AGGTGCATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325
QY 1281 GCCCATGTCGCCGAAAGTCTGCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1340
Db 326 ACCAATGTCGCGAAAGTCTGCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 385
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Db 386 CATCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
QY 1401 CGTGAGGAGCGCATCACCGGAGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1460
Db 446 TGTTCAGAAAGCCATCACTGAGACAGAGCATCAAGGCTGCTGCTGCTGCTGCTGCTG 505
QY 1461 CTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1520
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QY 1521 GCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580
Db 566 AGCGGCGCATGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625
QY 1581 CATCTCTCAGGTGATCATCGGCTGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTG 1640
Db 626 CATCTCTCAGGTGATCATCGGCTGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTG 685
QY 1641 CAACATCCCGGCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1700
Db 686 GAACATCCCGGCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745
QY 1701 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1755
Db 746 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 800
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Search completed: November 7, 2004, 14:38:30  
Job time : 1044 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 05:29:17 ; Search time 6565 Seconds  
(without alignments)  
11589.666 Million cell updates/sec

Title: US-09-679-687B-1  
Perfect score: 2088  
Sequence: 1 GCAAGACACCTCACTT.....AAAAAAAAAAAAAAAAAAAAA 2088

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues  
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsl:\*  
9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2088	100.0	2088	3	AY106212 Zea mays
2	850.6	40.7	902	6	CD440318 EL01N0553
3	790.4	37.9	895	6	CD441187 EL01N0553
4	630.6	30.2	1071	7	CK162307 FGAS01551
5	546	26.1	869	6	CD434724 EL01N0327
6	539.6	25.8	847	6	CB647418 OSUNEB10F
7	531.8	25.5	654	6	CA195914 SCEZAD108
8	523.6	25.1	705	5	BU925783 MCSA174E1
9	518.6	24.8	811	6	CB659941 OSUNED01E
10	516.4	24.7	843	6	CB661694 OSUNED04P
11	508	24.3	638	6	CD236385 SSI_33_G1
12	495	23.7	589	6	CA399941 EL01N0327
13	493.8	23.6	769	6	CB678068 OSUNEE15J
14	490.8	23.5	742	6	CB618707 OSITEA02M
15	488.8	23.4	719	5	BU925792 MCSA179A0
16	484.8	23.2	496	5	BQ538253 MEST599-A
17	480.2	23.0	581	2	BE361547 DGL_81_H0
18	476.8	22.8	657	6	CF325368 JMT1--04-
19	463	22.2	998	7	CK162767 FGAS01536
20	457.2	21.9	694	6	CD881813 FI.104E23
21	445	21.3	538	6	CA220149 SCRFL402
22	443.8	21.3	657	7	CNI50206 WOUND1_67
23	437.6	21.0	656	6	CD879901 AZO4_106L
24	433.8	20.8	539	6	CA163799 SCRURZ308

25	433.2	20.7	704	6	CD884481	CD884481 FL116M07
26	432.4	20.7	594	2	BF478755	BF478755 WHE2013_C
27	429	20.5	532	7	CF630902	CF630902 zmrws48_0
28	429	20.5	647	1	AV925143	AV925143 AV925143
29	425.8	20.4	533	7	CK369825	CK369825 zmrws485
30	422.6	20.2	592	5	BQ743802	BQ743802 WHE4108_C
31	422.4	20.2	526	6	CD970384	CD970384 QAD16e05
32	422.4	20.2	526	6	CD970430	CD970430 QAD17b09
33	420.6	20.1	617	4	BJ477966	BJ477966 BJ477966
34	416.4	19.9	482	4	BG837732	BG837732 Zm10_05d0
35	414.2	19.8	700	1	AL508285	AL508285 ALS08285
36	411.8	19.7	518	2	BE360821	BE360821 DGI_67_H0
37	411.6	19.7	828	4	BI953334	BI953334 HVSMEM001
38	411.4	19.7	795	7	CO522314	CO522314 3530_1_14
39	411.2	19.7	828	9	CO692415	CO692415 OGUCF61TH
40	409.8	19.6	768	7	CO527407	CO527407 3530_1_18
41	409.4	19.6	731	7	CK124551	CK124551 BES182410
42	403.8	19.3	587	6	CA222528	CA222528 SCBGPL405
43	402.4	19.3	516	7	CK371610	CK371610 zmrww005
44	396.2	19.0	757	8	BZ638091	BZ638091 OGCA67TC
45	393	18.8	582	6	CD057532	CD057532 HO15G16S

## ALIGNMENTS

RESULT 1  
AY106212  
LOCUS Zea mays PC0103031 mRNA sequence.  
DEFINITION Zea mays PC0103031 mRNA sequence.  
ACCESSION AY106212  
VERSION AY106212.1 GI:21209290  
KEYWORDS HTC.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 2088)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.  
AUTHORS Hayne, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 2 (bases 1 to 2088)  
Coe, E.H.

JOURNAL Direct Submission  
AUTHORS Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES  
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/clone\_lib="Maize Mapping Project/Dupont Consensus Library"  
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 100.0%; Score 2088; DB 3; Length 2088;





QY 1144 ATGGGCCGGAGATCTACCAAGCGGACCCCAAGGGAGCAACGCCGATCTCGGGGTTT 1203





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REFERENCE
AUTHORS      Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
              Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE        Large-scale identification of ESTs involved in the interaction
              between rice and Magnaporthe grisea
JOURNAL      Unpublished (2003)
COMMENT      Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967
              Fax: 520 621 9288
              Email: http://genome.arizona.edu
PCR Primers  FORWARD: gta aac cga cgg cca gtc
              BACKWARD: gga aac agc tat gac cat g
              Plate: 10 row: F column: 12
              Seq primer: gta aac cga cgg cca gtc.
              Location/Qualifiers
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            /db_xref="taxon:39947"
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            /tissue_type="Leaf"
            /dev_stage="3 week"
            /lab_host="DH10B"
            /clone_lib="OSJNEB"
            /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
            XhoI; 24 hrs after inoculation with Rice Blast (Che
            86061)"

ORIGIN
Query Match      25.8%; Score 539.6; DB 6; Length 847;
Best Local Similarity 78.0%; Pred. No. 2.8e-97;
Matches 663; Conservative 0; Mismatches 184; Indels 3; Gaps 1;

QY      698  ACTGTGCGAGTCCAGCAGCTGATGATGCTGATCTATGTGACCATCATGACCATCAGGCGCAAGT 747
DB      1  AATTTCTAGGGTCCAGCAGCTGCTTAAGGCTGATTTATCAGACGTCATGACCTGGC 60
QY      748  GCGGTACTCTCTCTCTGTTCTTGATGGCGCTGGGAACATCTTAGGCTACTCTCT 807
DB      61  ACAGTACTCTCTCTCTGTTCTTGATGGCAATGGGAACATCTTAGGATCTCTCT 120
QY      808  GGCTCAGCAAAATGGCAGACAGTGGTTCCCTTCCTTAAACGAGCGCTGCTGTGAG 867
DB      121  GGTTCACAAACAAATGGCAGAGTGGTTCCATTCCTTAAACGAGCTGTCTGAAA 180
QY      868  GCGTGTGCAACTCAAGGTGCATTTCTGTGGCGGTGGTTCCTAGTCTCTGTGCTG 927
DB      181  GTTGTGCAATTTGAAGGTGCATTTCTGTGGCTGTGATTTTCTCTGCTGCTGCTG 240
QY      928  ACGGTAACCTCTGATTTTCCCAAGAGGTGCGGTACAGAGCGACGAGAACCTCCGACG 987
DB      241  GTTATAACTCTGATATTTGCCAAGAGTTCATTTCAAAGAAATGACGCGCTCC---CA 297
QY      988  ACGAAGGCGCGGCGAGTCCAGACTGAGCTACCGGGCCACTTGGCTGCTCAAGGGC 1047
DB      298  ACAAAATCAACAGCAGCAGTGAAGCTGAGCACTGTCCTAGCAGTGTGAAGGC 357
QY      1048  TTCAAGGACCTCCCTCCCGGATGCGGTCCGCTGCTCTGCTGCTGCTGCTGCTGCT 1107
DB      358  TTCAGAACTTACCTACTGGAGTGCCTTCTGTGCTTATTGTGACTGGCTTACCTGTTG 417
QY      1108  TCGTGGTTCCTCTCTATCTCTACACACCGACTGGATGGCGGAGATCTACACAGGC 1167
DB      418  TTTTGGTTCCTCTCTATCTCTTACACACTGACTGGATGGCGGCTGAGATCTACACGGT 477
QY      1168  GACCCCAAGGAGCAACGCCCACTCTCGCGTTTCAACGAAAGTGTCCGAGTCCGCGCG 1227

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DB      478  GACCAAGGGAACATGATCCTCAGATCGAGGCTTTCAACAGGGTGTGTCAGGCGAGTGCA 537
QY      1228  TTCCGGCTGCTACTCAATCGGTTATTTAGGTTTCACTGCTGCTGATCGAGCCCATG 1287
DB      538  TTTGGCTGCTACTGAATTCGATTTGCTAGGATTCAGTTCATTTCTGATTGAACCAATG 597
QY      1288  TCCCGAAGGTCCGCGGAGGTGGTGGTGACGAGCAACTTCATGCTCTGGTGGTGGC 1347
DB      598  TCCCGAAGGTCCGCGGAGGTGGTGGTGACGAGCAACTTCCTGCTGTGATCGCC 657
QY      1348  ATGCGGGCCACCGCGCTGATCAGCTTCTGGTGGTTCAGGGACTACCGGGTACGTGCGAG 1407
DB      658  ATGGCTGCAACTGCACTGATCAGCTTCTGGTCACTCAAGGACTTCATGGAACCTGTT 717
QY      1408  GAGGCATCACCGCAGACCGCAGCATCAAGCGCTCAAGCGCTCTGCTGCTCTGCTCTG 1467
DB      718  AAAGCCATCAGTCGACAGCAAGAGCATCAAGGCTGTCTGCTGCTGCTCTGCTGCTT 777
QY      1468  GCGCTCCCTCTCGCCATCCTGTACAGCGTCCCGTTCGCGGTGACGCGCAGCTGCGGCC 1527
DB      778  GAGTCCCTCTCGCGTTCGTGTACAGTGTTCCTTCGCAGTGACGCGCGCAATAGCGGCC 837
QY      1528  ACCCGGGCG 1537
DB      838  ACTAGAGGGG 847

RESULT 7
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LOCUS      SCEZAD1082D06.g AD1 Saccharum officinarum cDNA clone SCEZAD1082D06
DEFINITION      5', mRNA sequence.
ACCESSION      CA195914
VERSION      CA195914.1 GI:35224640
KEYWORDS      EST
SOURCE      Saccharum officinarum
ORGANISM      Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
            complex.
REFERENCE      1 (bases 1 to 654)
AUTHORS      Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE      The libraries that made SUCEST
JOURNAL      Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT      Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bccccenter.fcav.unesp.br
            Plate: 082 row: D column: 06
            Seq primer: T7 Promoter Primer.
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            seedlings inoculated with Gluconacetobacter
            diazotrophicans). cDNA was prepared from polyA+ mRNA using
            Superscript Plasmid System Kit (Invitrogen). The
            double-strand cDNAs were fractionated in a sepharose
            CL-2B 40cm-columns and fragments sizing between 0.8 and

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[REDACTED]

\_\_\_\_\_

ORIGIN		Query Match 24.3%; Score 508; DB 6; Length 638; Best Local Similarity 89.2%; Pred. No. 5.7e-91; Matches 571; Conservative 0; Mismatches 65; Indels 4; Gaps 2;
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QY	862	TGTGAGGCTGTGGAACCTGAAAGGTGCAATTC-TGGTGGCCGTGGTGTCTTAGTCCT 920
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QY	921	GTGCTGACGTTACCTGTATCTTCGCCAAGAGGTGCCGTACAGAGGACAGACCT 980
Db	62	ATGCTTGGCTATAACCTTCGCTTCGCCAAGAAAGTACCATACAGAGAAACGAGAACCT 121
QY	981	CCCAGCAGAGGCGCGGCGAGGTGAGACTACGCTACCGGCGCACTTGCCTGCT 1040
Db	122	CC--CAACAAAGCAACGGGAGGTGAACTGAACCTACCGGCGCACTTGTGTGCT 178
QY	1041	CAAGGGCTTCAAGGACCTGCTCCCGGATCCGCTGCTCTCTGAGTGCCTATCAC 1100
Db	179	CAAGGGCTTCAAGAACTTGGCCCGGGATGCCATCCCTTCTCTGTAATGCGCCTCAC 238
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QY	1221	CGCGCGTTCGGGCTGCTACTCAACTCGTTATTTAGGGTTACGCTGTTCTCTGATCGA 1280
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QY	1341	CTGCGCATGCGGGCACCGCGCTGATAGCTTCTGCTGCTCAGGAGTACCGCGGTA 1400
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QY	1401	CTGCGAGGACCATCACCGCAACCGCAGATCAAGCGGCTCGCTCGCTTCTGCTGCG 1460
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QY	1461	CTTCTTGGCGCTCCCTCTCCCATCTGTGACAGCTCCCG 1500
Db	599	CTTCTTGGGTGCTCTCTCCCATCTGTGACAGCTCCCG 638
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DEFINITION		589 bp mRNA
ACCESSION		CA399941
VERSION		CA399941.1 GI:24764779
KEYWORDS		EST.
SOURCE		Zea mays
ORGANISM		Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 589); Lai,J., DeV.N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and Messing,J. Sequencing of the maize endosperm ESTs Unpublished (2002) Contact: Lai, Jinsheng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
RESULT 13		CB678068
LOCUS		OSUNBe15u24.f OSUNBe Oryza sativa (japonica cultivar-group) cDNA
DEFINITION		clone OSUNBe15u24 5', mRNA sequence.
ACCESSION		CB678068
VERSION		CB678068.1 GI:29681793
KEYWORDS		EST.
SOURCE		Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; Oryza.
ORGANISM		



```

REFERENCE
AUTHORS Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE Large-scale identification of ESTs involved in the interaction
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 15 row: J column: 24
Seq primer: gta aaa cga cgg cca gtc.
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Best Local Similarity 77.6%; Pred. No. 3.9e-88;
Matches 597; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
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QY 251 GGGGGCGCGCGGTGTGTGACACAGTGGCCCGCATGAGCTCGGAGGCTCATCTCG 310
Db 61 GTGAGCGCGCGCGGTGTGTGACACAGTGGCGGGCGGGCGGGCGGTGTGGGGAGGCTCT 120
QY 311 CGGGATGTGCTCGCGCGCGGTGTGTGACACAGTGGCGGGCGGTGTGGGGAGGCTCT 370
Db 121 CGGGATGTGCTCGCGCGCGGTGTGTGACACAGTGGCGGGCGGTGTGGGGAGGCTCT 180
QY 371 CCTAGTGCAGACTGTGGGGCTTTTACATGGCGCTCACTTCATTCATGTGGCTCTGCGGCC 430
Db 181 CCTAGTGCAGACTGTGGGGCTTTTACATGGCGCTCACTTCATTCATGTGGCTCTGCGGCC 240
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Db 241 CTATTGCTGGAGTGTGTGTTCAACATGCGTGGGTCTTACAGTGTAGGTGCACTCAA 300
QY 491 GATGGGGAGACGAGGGCGGTTTATCTGACAGGGTGCATGCTCATCTGCGTTGCGGTCFA 550
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Db 541 GAGCTCATGGACCTGGCACAGCTAACTCTCTTGTGATGGCAATGGGAACA 600
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Db 661 CAAGAGCTTGTGTGAGCTTGTGCAATTTTGAAGTGTGCAATTTCTGGTGGCTGTGATTT 720
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Db 721 TCTTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
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LOCUS CB618707 742 bp mRNA linear EST 08-APR-2003
DEFINITION OSIIIEa02M22.f OSIIIEa Oryza sativa (indica cultivar-group) cDNA
clone OSIIIEa02M22 5', mRNA sequence.
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VERSION CB618707.1 GI:29613694
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SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaceae; Oryza.
1 (bases 1 to 742)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: M column: 22
Seq primer: gta aaa cga cgg cca gtc.
FEATURES
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Query Match 23.5%; Score 490.8; DB 6; Length 742;
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Matches 579; Conservative 0; Mismatches 147; Indels 0; Gaps 0;
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 LOCUS  
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ACCESSION  
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 VERSION  
 BU925792.1  
 KEYWORDS  
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 SOURCE  
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ORGANISM  
 Saccharum sp.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE  
 1 (bases 1 to 719)  
 Casu, R.E., Grof, C.P.L., Rae, A.L., McIntyre, C.L., Dimmock, C.M. and Manners, J.M.  
 Identification of a novel sugar transporter homologue strongly expressed in maturing stem vascular tissues of sugarcane by expressed sequence tag and microarray analysis  
 Plant Mol. Biol. 52 (2), 371-386 (2003)

JOURNAL  
 MEDLINE  
 22740593  
 PUBMED  
 12856943  
 CONTACT: Rosanne E. Casu

Commonwealth Scientific and Industrial Research Organisation  
 Division of Plant Industry  
 Long Pocket Laboratories, 120 Meiers Rd, Indooroopilly, QLD, 4068,  
 Australia  
 Tel: 61 7 3214 2364  
 Fax: 61 7 3214 2881  
 Email: Rosanne.Casu@csiro.au  
 Bases 1-17 (GTCGACCCACGCTCCG): Sali adapter  
 Seq primer: T7 sequencing primer  
 High quality sequence stop: 719.

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 258 CTTTCCTTAAACAGGCGCTGCTGAGGCTGCGGACCTGGAAGTGCATTTCTGGT 317  
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